

Amendments to the Specification

At the indicated page and line numbers, please replace the existing paragraph with the one set forth below.

(Page 23, lines 9-13)

The genes of Table S6 are listed with their Unigene accession numbers corresponding to Build 160 of the Unigene database. The sequence of each gene can therefore be retrieved from the Unigene database at the National Institute of Health (NIH): (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene> www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene).

(Page 23, lines 15-22)

Furthermore, for all of the genes, Affymetrix (Santa Clara, Calif.) (~~www.affymetrix.com~~ www.affymetrix.com) provide examples of probe sets, including the sequences of the probes, (i.e. binding members in the form of oligonucleotide sequences) that are capable of detecting expression of the gene when used on a solid support. The probe details are accessible from the U133A section of the Affymetrix website using the Unigene ID of the target gene.

(Page 56, line 25 through page 57, line 2)

Stanford Data Set: A similar approach was used to test the NPI-ES on the Stanford data set (see Fig. S10). Of the SAM-409 gene set used to define the ER+, ER-, and ERBB2+subtypes, 136 genes were found on the Stanford microarray (~~<http://genome-www5.stanford.edu/MicroArray/SMD/>~~ genome-www5.stanford.edu/MicroArray/SMD/), and these genes were used to cluster the Stanford tumours to identify 46 tumours belonging to the ER+ molecular subtype (from 72 tumors after discarding the normal-like tumor subgroup of 6 tumors, which subgroup is likely to be due to the presence of contaminating non-malignant tissue).